

OM protein - protein search, using sw model

Run on: August 18, 2005, 09:38:49 ; Search time 79 Seconds
(without alignments)
842.061 Million cell updates/sec

Title: US-10-021-753A-2
Perfect score: 172
Sequence: 1 MIIYRDLISHDEMFSDIYKI.....EDGVTPYMIFFKDGLEMEKC 172

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 20

Total number of hits satisfying chosen parameters: 37

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	172	100.0	172	2	AAR55698	Aar55698 Tumor pro
2	172	100.0	172	5	AAU97773	Aau97773 Human For
3	172	100.0	172	6	ABR44810	Abr44810 Human TCP
4	172	100.0	172	6	ABU07429	Abu07429 Protein d
5	172	100.0	172	6	ABU11888	Abu11888 Human ABC
6	172	100.0	172	7	ADD26671	Add26671 Human adi
7	172	100.0	172	7	ADE61268	Ade61268 Human Pro
8	172	100.0	172	7	ADG10760	Adg10760 Human STA
9	172	100.0	172	8	ADP82721	Adp82721 Human for

10	172	100.0	172	8	ADQ30542	Adq30542	Pancreas
11	172	100.0	172	8	ABM81514	Abm81514	Tumour-as
12	172	100.0	182	7	ADE09075	Ade09075	Novel pro
13	172	100.0	197	5	ABB97354	Abb97354	Novel hum
14	153	89.0	208	7	ADE08040	Ade08040	Novel pro
15	138	80.2	146	4	ABG26035	Abg26035	Novel hum
16	130	75.6	215	2	AAR05882	Aar05882	Sequence
17	108	62.8	110	4	ABG26036	Abg26036	Novel hum
18	108	62.8	111	4	AAU29787	Aau29787	Novel hum
19	98	57.0	172	5	AAU79211	Aau79211	Human tum
20	92	53.5	108	4	ABG26034	Abg26034	Novel hum
21	78	45.3	172	5	AAU79307	Aau79307	Human tra
22	62	36.0	189	4	AAU29788	Aau29788	Novel hum
23	52	30.2	86	5	ABP42338	Abp42338	Human ova
24	52	30.2	120	4	ABG26033	Abg26033	Novel hum
25	35	20.3	74	8	ADS12214	Ads12214	Human the
26	35	20.3	191	4	ABG26037	Abg26037	Novel hum
27	31	18.0	172	5	ABB83345	Abb83345	Murine TS
28	31	18.0	172	5	ABB83346	Abb83346	Human TSA
29	31	18.0	172	5	AAU79212	Aau79212	Murine tu
30	31	18.0	172	5	AAU79210	Aau79210	Murine tu
31	31	18.0	172	7	ADE61266	Ade61266	Rat Prote
32	30	17.4	190	8	ABM80805	Abm80805	Tumour-as
33	26	15.1	138	8	ABM81068	Abm81068	Tumour-as
34	24	14.0	140	8	ADR08494	Adr08494	Human pro
35	21	12.2	21	2	AAR60844	Aar60844	COSM prec
36	21	12.2	22	5	AAU97774	Aau97774	Synthetic
37	20	11.6	34	5	ABB83347	Abb83347	Murine TS

ALIGNMENTS

RESULT 1

AAR55698

ID AAR55698 standard; protein; 172 AA.

XX

AC AAR55698;

XX

DT 25-MAR-2003 (revised)

DT 16-NOV-1994 (first entry)

XX

DE Tumor protein p21.

XX

KW Transcriptionally controlled tumor protein p21; TCTPp21; tumor marker;

KW ELISA; immunoassay; DNA probe; hybridization; breast cancer;

KW ovary cancer; cervix cancer; prostate cancer; colon cancer; diagnosis.

XX

OS Homo sapiens.

XX

PN W09412881-A2.

XX

PD 09-JUN-1994.

XX

PF 26-NOV-1993; 93WO-EP003314.

XX

PR 02-DEC-1992; 92US-00990302.

GenCore version 5.1.6
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Run on: August 18, 2005, 06:30:09 ; Search time 2889 Seconds
(without alignments)

Perfect score: 830

Gapop 60.0 , Gapext 60.0

Word size : 20

Minimum DB seq length: 0

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA*

- 1: *cgrr2_6fpodata2/pubnpa/US507_PUBCOMB.seq**
2: *cgrr2_6fpodata2/pubnpa/PTC1_NEW_PUB.seq**
3: *cgrr2_6fpodata2/pubnpa/US506_NEW_PUB.seq**
4: *cgrr2_6fpodata2/pubnpa/US06_PUBCOMB.seq**
5: *cgrr2_6fpodata2/pubnpa/US07_NEW_PUB.seq**
6: *cgrr2_6fpodata2/pubnpa/PTUS_PUBCOMB.seq**
7: *cgrr2_6fpodata2/pubnpa/US08_NEW_PUB.seq**
8: *cgrr2_6fpodata2/pubnpa/US09_PUBCOMB.seq**
9: *cgrr2_6fpodata2/pubnpa/US09A_PUBCOMB.seq**
10: *cgrr2_6fpodata2/pubnpa/US09B_PUBCOMB.seq**
11: *cgrr2_6fpodata2/pubnpa/US09C_PUBCOMB.seq**
12: *cgrr2_6fpodata2/pubnpa/US09_NEW_PUB.seq**
13: *cgrr2_6fpodata2/pubnpa/US10A_PUBCOMB.seq**
14: *cgrr2_6fpodata2/pubnpa/US10_PUBCOMB.seq**
15: *cgrr2_6fpodata2/pubnpa/US10C_PUBCOMB.seq**
16: *cgrr2_6fpodata2/pubnpa/US10D_PUBCOMB.seq**
17: *cgrr2_6fpodata2/pubnpa/US10E_PUBCOMB.seq**
18: *cgrr2_6fpodata2/pubnpa/US10F_PUBCOMB.seq**
19: *cgrr2_6fpodata2/pubnpa/US10G_PUBCOMB.seq**
20: *cgrr2_6fpodata2/pubnpa/US10H_PUBCOMB.seq**
21: *cgrr2_6fpodata2/pubnpa/US10_PUBCOMB.seq**
22: *cgrr2_6fpodata2/pubnpa/US10_NEW_PUB.seq**
23: *cgrr2_6fpodata2/pubnpa/US11A_PUBCOMB.seq**
24: *cgrr2_6fpodata2/pubnpa/US11_NEW_PUB.seq**
25: *cgrr2_6fpodata2/pubnpa/US60_NEW_PUB.seq**
26: *cgrr2_6fpodata2/pubnpa/US60_PUBCOMB.seq**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES	
%	Query
Result	

No.	Score	Match	Length	DB ID	Description
1	830	1000	830	9 US-09-968-708-101	Sequence 101, App
2	830	1000	830	14 US-10-153-668-349	Sequence 349, App
3	830	1000	830	16 US-10-021-753-1	Sequence 1, App
4	830	1000	830	21 US-10-843-614-1-7572	Sequence 1572, App
5	830	1000	830	21 US-10-965-151-1044	Sequence 1044, App
6	830	1000	830	21 US-10-966-165-6279	Sequence 6279, App
7	810	976	810	21 US-10-800-322-330	Sequence 320, App
8	622	749	623	20 US-10-684-422-33	Sequence 33, App
9	590	711	590	9 US-09-998-598-1343	Sequence 1343, App
10	577	695	599	9 US-09-919-580-88	Sequence 88, App
11	543	654	976	20 US-10-128-555-1	Sequence 71, App
12	539	649	539	17 US-10-242-553A-16379	Sequence 16379, App
13	539	641	539	18 US-10-005-783A-16379	Sequence 16379, A
14	532	641	532	9 US-09-999-598-1274	Sequence 1274, App
15	519	625	519	17 US-10-139-794-5	Sequence 5, App
16	519	625	519	18 US-10-439-298-6	Sequence 6, App
17	519	625	577	9 US-09-919-580-46	Sequence 466, App
18	496	598	506	9 US-09-920-465-187	Sequence 187, App
19	480	578	531	9 US-09-920-300A-1003	Sequence 1004, App
20	480	578	531	13 US-10-034-528-1004	Sequence 1004, App
21	480	578	531	16 US-10-069-996-1004	Sequence 1004, App
22	480	578	531	22 US-10-961-527-1004	Sequence 1004, App
23	475	572	499	17 US-10-242-553A-58441	Sequence 58441, A
24	475	572	499	18 US-10-085-783A-58441	Sequence 58441, A
25	474	571	535	9 US-09-920-300A-710	Sequence 710, App
26	474	571	535	13 US-10-033-528-710	Sequence 710, App
27	474	571	535	16 US-10-069-996-710	Sequence 710, App
28	474	571	535	22 US-10-961-527-710	Sequence 710, App
29	470	566	465	17 US-09-999-599-1025	Sequence 1025, App
30	465	560	465	17 US-10-242-553A-36210	Sequence 36210, App
31	465	560	465	17 US-10-242-553A-37978	Sequence 37978, A
32	465	560	465	18 US-10-085-783A-36210	Sequence 36210, A
33	465	560	465	18 US-10-085-783A-37978	Sequence 37978, A
34	465	560	703	11 US-09-966-594-4221	Sequence 4221, App
35	461	555	490	9 US-09-999-599-459	Sequence 459, App
36	468	551	508	9 US-09-918-995-21311	Sequence 21311, App
37	467	551	468	13 US-09-878-178-1174	Sequence 1174, App
38	467	551	468	13 US-10-146-502-1174	Sequence 1174, App
39	467	551	468	14 US-10-166-802-1174	Sequence 1174, App
40	456	549	464	9 US-09-878-178-244	Sequence 244, App
41	456	549	464	13 US-10-146-502-244	Sequence 244, App
42	456	549	465	17 US-10-242-553A-44226	Sequence 44226, A
43	453	546	465	17 US-10-085-783A-44226	Sequence 44226, A
44	453	546	465	18 US-10-085-783A-44226	Sequence 44226, A
45	452	545	502	10 US-09-918-995-209520	Sequence 20950, App

ALIGNMENTS

RESULT 1

; Sequence 101, Application US/09969708

; Patent No. US20020102532A

GENERAL INFORMATION:

AFRICANA: Augustus, Meena

: TITLE OF INVENTION: Sets

FILE REFERENCE: 689290-70

: CURRENT APPLICATION NUMBER

CURRENT FILING DATE: 200

PRIORITY APPLICATION NUMBER:

PRIOR FILING DATE: 2000-10-11

APPLICATION NUMBER

TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signature Gene

: FILE OF INVENTION. SEE
: FILE REFERENCE. 680390-70

CURRENT APPLICATIONS

CURRENT FILING DATE: 200

; PRIOR APPLICATION NUMBER

; PRIOR FILING DATE: 2000-10

; PRIOR APPLICATION NUMBER

XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX Rokuten K;
XX WPI; 2002-362309/39.
DR N-PSDB; ABK49328.
XX
PT Insulin secretion-controlling agents acting on IGF-dependent histamine-
releasing factors, useful in diagnosis and drugs for e.g. diabetes,
obesity, edema and insulinoma.
XX
XX Example; Page 82-83; 89pp; Japanese.
XX
XX The invention relates to insulin-secretion controlling agents. IGF-
dependent histamine releasing factors (IGF-dependent HRFs) such as tumour
-associated protein (TCP) are controlling factors for insulin secretion
from pancreatic beta cells and are therefore useful as insulin secretion
inhibitors. Substances inhibiting the effect of IGF-dependent HRFs are
useful as insulin secretion promoters and preventives and remedies for
diabetes. The agents are useful in diagnosis and production of drugs for
treatment of disorders such as diabetes, insulin secretion failure,
resistance to sugar, ketosis, acidosis, diabetic neural disorders,
diabetic nephropathy, diabetic omentopathy, hyperlipaemia, sexual
dysfunction, skin diseases, arthritis, bone reduction, obesity, type II
diabetes, hypoglycaemia, hypertension, edema, insulin resistance,
unstable diabetes, lipotrophy, insulin allergy and insulinoma. This
sequence represents human TCP p23
XX
SQ Sequence 172 AA:
Query Match 99.88; Score 896; DB 5; Length 172;
Best Local Similarity 99.48; Pred. No. 8.5e-88;
Matches 171; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MIIYRDLISHDEMFSDIYKIRIADGICLVEGKVSRTGKIDSLIGNSAAGEEG 60
DB 1 MIIYRDLISHDEMFSDIYKIRIADGICLVEGKVSRTGKIDSLIGNSAAGEEG 60
QY 61 GTESTVITGVDIVNHHLOETSFTEKAYKKYIKDYMSIKGLBQRPENVPMTGAE 120
DB 61 GTESTVITGVDIVNHHLOETSFTEKAYKKYIKDYMSIKGLBQRPENVPMTGAE 120
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DB 121 QIKHILANFNKYQFFIGENNPDGVALLDYREDGVTPYMFIFKDGLEMEKC 172
RESULT 15
ABB83345
ID ABB83345 standard; protein; 172 AA.
XX
AC ABB83345;
XX
DT 02-SEP-2002 (first entry)
XX
DE Murine TSA6 binding protein #19.
XX
KW Neuroprotective; cytosolic; TSA6; apoptosis; cancer; neurodegeneration;
tumour suppressor Activated Pathway 6; TSA6 binding protein; tumour;
murine; human.
XX
OS Mus musculus.
XX
PN WO200252274-A2.
XX
PD 04-JUL-2002.
XX
PF 24-DEC-2001; 2001WO-FR004188.
XX

PR 26-DEC-2000; 2000FR-00017027.
PR 18-SEP-2001; 2001WO-FR002896.
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Amson R, Teberman A, Passer B;
XX WPI; 2002-508914/54.
DR
XX
PT Identifying compounds that inhibit binding of TSA6 to proteins for
treating cancer and neurodegeneration.
XX
XX Claim 1; Page 58-59; 79pp; French.
XX
XX The present invention relates to a method for identifying a compound (1)
that inhibits binding of TSA6 (Tumour Suppressor Activated Pathway) 6 to
a TSA6 binding protein. The present sequence is one such TSA6 binding
protein. (1) are useful for modulating tumour reversal and/or apoptosis
for treating cancer or neurodegeneration
XX
SQ Sequence 172 AA:
Query Match 97.18; Score 872; DB 5; Length 172;
Best Local Similarity 95.98; Pred. No. 3.2e-85;
Matches 165; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
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DB 1 MIIYRDLISHDEMFSDIYKIRIADGICLVEGKVSRTGKIDSLIGNSAAGEEG 60
QY 61 GTESTVITGVDIVNHHLOETSFTEKAYKKYIKDYMSIKGLBQRPENVPMTGAE 120
DB 61 GTESTVITGVDIVNHHLOETSFTEKAYKKYIKDYMSIKGLBQRPENVPMTGAE 120
QY 121 QIKHILANFNKYQFFIGENNPDGVALLDYREDGVTPYMFIFKDGLEMEKC 172
DB 121 QIKHILANFNKYQFFIGENNPDGVALLDYREDGVTPYMFIFKDGLEMEKC 172
Search completed: August 18, 2005, 09:38:21
Job time : 323 secs
GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.
OK protein - protein search, using sw model
Run on: August 18, 2005, 08:44:23 ; Search time 117 Seconds
(without alignments)
109.741 Million cell updates/sec
Title: US-10-021-753A-2
Perfect score: 898
Sequence: 1 MIIYRDLISHDEMFSDIYKIRIADGICLVEGKVSRTGKIDSLIGNSAAGEEG 172
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 513545 seqs, 74649064 residues
Total number of hits satisfying chosen parameters: 513545
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/aa/5b.CONB.pep:*
- 3: /cgn2_6/ptodata/1/aa/5c.CONB.pep:*
- 4: /cgn2_6/ptodata/1/aa/5d.CONB.pep:*
- 5: /cgn2_6/ptodata/1/aa/5e.CONB.pep:*
- 6: /cgn2_6/ptodata/1/aa/5f.CONB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	898	100.0	182	4	US-09-949-016-9957
2	870	96.9	172	3	US-09-311-311C-27
3	844	92.8	191	4	US-09-270-767-43182
4	371	41.3	167	2	US-08-690-849-2
5	371	41.3	167	3	US-09-004-053-2
6	347.5	38.7	196	4	US-09-248-796A-14442
7	267	29.7	168	4	US-09-737-300-2
8	170.5	19.0	107	4	US-09-270-767-39492
9	170.5	19.0	107	4	US-09-270-767-54709
10	114	12.7	21	3	US-08-105-904B-12
11	114	12.7	21	3	US-08-114-877A-12
12	107	11.9	21	3	US-08-537-928-12
13	107	11.9	21	4	US-09-633-269-12
14	82	9.5	332	4	US-09-248-796A-15783
15	82	9.5	459	4	US-09-489-039A-7416
16	81.5	9.1	593	4	US-09-949-016-6071
17	81.5	9.1	593	4	US-09-949-016-10192
18	81.5	9.1	759	4	US-09-328-352-7650
19	81.5	9.1	1023	4	US-09-762-724-14
20	80.5	9.0	1017	4	US-09-762-724-12
21	80	8.9	16	2	US-08-658-639-2
22	80	8.9	16	3	US-08-944-604-2
23	79.5	8.9	1391	4	US-10-080-505-11
24	79.5	8.9	1391	4	US-10-080-505-15
25	78	8.8	449	4	US-09-603-208A-42
26	78	8.7	256	3	US-09-134-001C-5211
27	77.5	8.6	331	4	US-09-744-072-2
28	77.5	8.6	1523	4	US-09-107-433-4771
29	77.5	8.6	2138	4	US-09-583-110-5274
30	77	8.6	438	4	US-09-589-510-10
31	76	8.5	251	4	US-09-107-532A-5242
32	76	8.5	1007	3	US-08-961-083-216
33	76	8.5	1007	4	US-09-536-784-216
34	75.5	8.4	231	3	US-08-961-083-176
35	75.5	8.4	231	4	US-09-536-784-176
36	75.5	8.4	511	4	US-09-248-796A-16380
37	75.5	8.4	872	1	US-08-451-115A-8
38	75.5	8.4	1027	1	US-09-762-724-8
39	75	8.4	231	2	US-08-969-721-8
40	75	8.4	328	4	US-09-902-540-10796
41	75	8.4	492	4	US-09-991-258-5
42	75	8.4	642	4	US-09-248-796A-15380
43	75	8.4	890	4	US-09-849-602-19
44	74.5	8.3	526	4	US-09-248-796A-16081
45	74.5	8.3	587	4	US-09-328-352-8096

ALIGNMENTS

RESULT 1
US-09-949-016-9957
; Sequence 9957, Application US/0949016

Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9957
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9957

Query Match 100.0%; Score 898; DB 4; Length 182;
Best Local Similarity 100.0%; Pred. No. 8.3e-88;
Matches 172; Conservative 0; Mismatches 0; Indels 0;

1 MIIYRDLISHDMFSDIYKRIEADGCLVEGKWSRTGNIIDSLIGNSAAGEEGE 60
|||||
11 MIIYRDLISHDMFSDIYKRIEADGCLVEGKWSRTGNIIDSLIGNSAAGEEGE 70
OY 61 GRESTVITGDIYVNNHLLQSTFTKEXKKYIKDYKRSIKGLBQRPENKRPYTGAAE 120
|||||
71 GRESTVITGDIYVNNHLLQSTFTKEXKKYIKDYKRSIKGLBQRPENKRPYTGAAE 130
OY 121 QIKHILANFKNYQFIFGENNPDGMVALLDYREDGVTPIYIFKDGLEMEKC 172
|||||
DB 131 QIKHILANFKNYQFIFGENNPDGMVALLDYREDGVTPIYIFKDGLEMEKC 182

RESULT 2
US-09-311-311C-27
; Sequence 27, Application US/09311311C
; Patent No. 6358738
; GENERAL INFORMATION:
; APPLICANT: Eliason, et al.
; TITLE OF INVENTION: FOLD BOX THERAPEUTIC COMPOSITIONS,
; FILE REFERENCE: 1874/117
; CURRENT APPLICATION NUMBER: US/09/311,311C
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,296
; PRIOR FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: DOMAIN
; LOCATION: (1)...(172)
; OTHER INFORMATION: TCTP/23 protein
US-09-311-311C-27

Query Match 96.9%; Score 870; DB 3; Length 172;
Best Local Similarity 97.7%; Pred. No. 7.4e-85;
Matches 168; Conservative 0; Mismatches 4; Indels 0;
OY 1 MIIYRDLISHDMFSDIYKRIEADGCLVEGKWSRTGNIIDSLIGNSAAGEEGE 60
|||||

ALIGNMENTS

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	898	100.0	172	1	TCRP_HUMAN	P13693 homo sapien
2	888	100.0	172	1	TCRP_PIG	P61288 sus scrofa
3	884	98.4	172	1	TCRP_RABIT	P13318 corycolaga
4	872	97.1	172	1	TCRP_MOUSE	P53028 mus muscula
5	872	97.1	172	1	TCRP_RAT	P63029 rattus norv
6	872	97.1	172	2	Q66GM6	Q66GM6 xenopus lae
7	831	92.5	172	1	TCRP_CHICK	P43347 gallus gall
8	803	89.4	155	2	Q862G3	Q862G3 bos taurus
9	723	80.5	138	2	Q8TRK7	Q8TRK7 homo sapien
10	643.5	71.7	173	1	FKG2_HUMAN	Q8HA6 homo sapien
11	635	70.7	172	2	Q66JG5	Q66JG5 xenopus tro
12	632.5	70.4	171	1	TCRP_LABRO	Q88517 labeo rohlt
13	628.5	70.0	171	1	TCRP_BRARE	Q8d9K4 brachydantio
14	627	69.8	172	2	Q7ZYF2	Q7ZYF2 xenopus lae
15	620.5	69.1	171	2	Q862H4	Q862H4 brachydantio
16	602	67.0	117	2	Q862H4	Q862H4 bos taurus
17	591	65.8	140	2	Q6ZT11	Q6ZT11 homo sapien
18	581	64.7	170	2	Q6XSH4	Q6XSH4 lacteolabrax
19	572	63.7	114	2	Q862L1	Q862L1 bos taurus
20	502	55.9	95	2	Q862X2	Q862X2 bos taurus
21	471.5	52.5	169	1	TCRP_BRARE	Q95VY2 brachyosteo
22	470	52.3	92	2	Q862N1	Q862N1 bos taurus
23	468	52.1	88	2	Q862V4	Q862V4 bos taurus
24	430	47.9	114	2	Q9UP43	Q9UP43 homo sapien
25	412	45.9	168	1	TCRP_SCHPO	Q10344 schistosach
26	409.5	45.6	167	2	Q6C4G1	Q6C4G1 yarrowia li
27	392	43.7	172	2	Q7SVN3	Q7SVN3 bombyx mori
28	387	43.1	172	2	Q6X1N1	Q6X1N1 dirosophila
29	384	42.8	172	1	TCRP_DROME	Q9VW32 dirosophila
30	372.5	41.5	412	2	Q9NMX1	Q9NMX1 homo sapien
31	371.5	41.4	185	2	Q6TCK2	Q6TCK2 anopheles g
32	366.5	40.8	167	2	Q6CTH3	Q6CTH3 kluyveromyc
33	362.5	40.4	167	2	Q6FKB6	Q6FKB6 candida gla
34	361.5	40.3	167	1	TCRP_LUMRU	Q18477 lumbricus r
35	358.5	39.9	167	1	TCRP_YEAST	P34691 saccharomyc
36	357	39.8	170	2	Q7RYV5	Q7RYV5 neurospora
37	355.5	39.6	169	1	TCRP_SCHJA	P18800 schistosoma
38	347.5	38.7	167	2	Q6BP09	Q6BP09 deparomyce
39	333	37.1	172	2	Q6BJR2	Q6BJR2 tigrisopus j
40	329	36.6	64	2	Q86YH5	Q86YH5 homo sapien
41	326	36.3	166	1	TCRP_SCMA	Q95W42 schistosoma
42	325	36.2	147	2	Q6XHY0	Q6XHY0 dirosophila
43	322	35.9	168	2	Q86GR2	Q86GR2 penaeus mon
44	319.5	35.6	173	2	Q879S3	Q879S3 demacentor
45	307.5	34.2	167	1	TCRP_MEDSA	P28014 medicago sa

ALIGNMENTS

RESULT 1
ID TCRP_HUMAN STANDARD: PRT: 172 AA.
AC P13693: Q6YLS2: Q7Z4J4: Q86EE2: Q9UC70:
DT 01-JAN-1990 (Rel. 13) Created
DT 01-JAN-1990 (Rel. 13) Last sequence update
DT 25-OCT-2004 (Rel. 45) Last annotation update
DE Translationally controlled tumor protein (TCRP) (p23) (histamine-releasing factor) (HRF).

GN Name=TP11;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_TaxID=9606;
NM (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=90045959; PubMed=2813067;
RA Gross B., Gaestel M., Boehm H., Bielek H.;
RT "CDNA sequence coding for a translationally controlled human tumor protein";
RL Nucleic Acids Res. 17:8367-8367(1989).
NM (2)
RP SEQUENCE FROM N.A.
RA Thiele H.;
RT Thesis (2000), Humboldt-University Berlin, Germany.
NM (3)
RP SEQUENCE FROM N.A.
RX Granasaker M., Ramaswamy K.;
RA "Cloning and characterization of TCRP from human eosinophils";
RT Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
NM (4)
RP SEQUENCE FROM N.A.
RX Gao T.H., Duan F.L., Zhu W.L.;
RA Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
NM (5)
RP SEQUENCE FROM N.A.
RX Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RA "Cloning of human full open reading frames in Gateway(TM) system entry vector (pDONR201)".
RT Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
NM (6)
RP SEQUENCE FROM N.A.
RX TISSUE=lung, and Placenta;
RA MEDLINE=22368257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strubeberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bahr S.S., Loguanello N.A., Peters G.J., Abramson R.D., Mulvaney S.J.,
RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.L., Skalska U., Smalins D.E.,
RA Schercher A., Schell J.E., Jones S.J.W., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences".
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
NM (7)
RP SEQUENCE OF 1-10.
RA TISSUE=livert;
RX MEDLINE=93162045; PubMed=1286669;
RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,
RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,
RA Appel R.D., Hughes G.J.;
RT "Human liver protein map: a reference database established by microsequencing and gel comparison".
RL Electrophoresis 13:992-1001(1992).
NM (8)
RP SEQUENCE OF 1-4; 22-31; 39-45 AND 103-109.
RA TISSUE=keratinocytes;
RX MEDLINE=93162043; PubMed=1286667;
RA Rasmussen H.H., van Damme J., Puyse M., Gesser B., Celis J.E.,

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Query Match          59.8%. Score 537; DB 16; Length 105;
Best Local Similarity 95.28; Pred. No. 8.3e-46;
Matches 100; Conservative 4; Mismatches 1; Indels 0; Gaps 0

QY      66 VITGVDVNNHHLDSTSTFEAKRYIKDYMSIKGLSEQRERKVFMTGAADIKHI 125
      1:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db       1 VWTGVDVNNHHLDSTSTFEAKRYIKDYMSIKGLSEQRERKVFMTGAADIKHI 60

QY      126 LANFKMYQVFIGENNNRPGXVALLDYREDGVPPYMIFFPKDLEME 170
      111|111|111|111|111|111|111|111|111|111|111|111|111|111|111|
Db       61 LANFKMYQVFIGENNNRPGXVALLDYREDGVPPYMIFFPKDLEME 105

Search completed: August 18, 2005, 09:56:41
Job time : 493 secs

                                GenCore version 5.1.6
                                Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on:      August 18, 2005, 08:41:19 ; Search time 71 Seconds
              (without alignments)
              233.088 Million cell updates/sec

Title:       US-10-021-753A-2
Perfect score: 898
Sequence:    1 MIYRDLTSHDEMSDIYKI.....EDGVTPMIFPKDLEMEKC 172

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:    283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :
1: PIR.79:*
2: p1r1:*
3: p1r2:*
4: p1r3:*
5: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result      #
No.         Query Match length DB ID Description
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1      898 100.0 172 1 S06590 IGF-dependent hist
2      872 97.1 172 1 S00775 IGF-dependent hist
3      862 96.0 172 1 A38956 IGF-dependent hist
4      831 92.5 172 1 A38960 IGF-dependent hist
5      412 45.9 168 2 S67445 IGF-dependent hist
6      358.5 39.9 167 1 S37878 IGF-dependent hist
7      307.5 34.2 167 2 T09686 TCPP protein homol
8      302.5 33.7 167 2 T06567 IGF-dependent hist
9      291 32.4 168 1 A38958 IGF-dependent hist
10     278.5 31.0 157 2 S22489 IGF-dependent hist
11     274 30.5 168 1 A39355 IGF-dependent hist

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12	256.5	28.6	181	2	T21352	hypothetical prote
13	92.5	10.3	537	2	T27612	hypothetical prote
14	90.5	10.1	870	2	G81348	valine-tRNA ligase
15	87.5	9.7	488	2	T10256	gag polyprotein ho
16	87	9.7	572	1	ERBP22	DNA-directed DNA p
17	87	9.7	575	1	ERBP22	DNA-directed DNA p
18	86.5	9.6	570	2	S55525	Ulp protein - mou
19	85	9.5	329	2	A33493	1-phosphatidylinos
20	85	9.5	1173	2	T25985	1-phosphatidylinos
21	84	9.4	329	2	A30760	1-phosphatidylinos
22	84	9.4	1787	2	T20160	hypothetical prote
23	83.5	9.3	468	2	B90568	atp synthase beta
24	83	9.2	496	2	T46356	hypothetical prote
25	82.5	9.2	598	2	H69011	hypothetical prote
26	81.5	9.1	590	2	A64549	conserved hypochet
27	81.5	9.1	570	2	JCS318	dihydropyrimidinas
28	81.5	9.1	1022	2	T30543	major surface glyco
29	81	9.0	1198	2	T42223	ladder protein - C
30	80.5	9.0	673	2	T44079	H+/K+-exchanging A
31	80.5	9.0	673	2	B89766	hypothetical prote
32	80.5	9.0	1017	2	T30542	major surface glyco
33	80	8.9	323	2	A86184	hypothetical prote
34	80	8.9	1073	1	T08228	plasmid replicatio
35	79	8.8	300	2	AF1115	transcription regu
36	79	8.8	341	2	S31236	hypothetical prote
37	79	8.8	745	2	S49155	heat shock protein
38	78.5	8.7	266	2	T41094	very hypothetical
39	78.5	8.7	304	2	G82940	hypothetical prote
40	78.5	8.7	872	2	E71852	valine-tRNA ligase
41	78.5	8.7	874	2	A64664	valine-tRNA ligase
42	78.5	8.7	900	2	B69631	galactosamine-cont
43	78	8.7	441	2	T25947	hypothetical prote
44	78	8.7	469	2	B70201	hypothetical prote
45	78	8.7	501	2	S54377	gag polypeptide -

ALIGNMENTS

RESULT 1
S06590
IGF-dependent histamine-releasing factor - human
N:Alternate names: 21K tumor protein; tumor-associated protein
C:Species: Homo sapiens (man)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S06590; A43082; F33178
R:Gross, B.; Gaestel, M.; Boehm, H.; Bielka, H.
Nucleic Acids Res. 17, 8367, 1989
A:Title: cDNA sequence coding for a translationally controlled human tumor protein.
A:Reference number: S06590; MUID:90045959; PMID:2813067
A:Accession: S06590
A:Molecule type: mRNA
A:Residues: 1-172 <GRO>
A:Cross-references: UNIPROT:P13693; EMBL:X16064; NID:g37495; PIDN:CAA34200.1;
PID:g37496
R:Macdonald, S.M.; Rafnar, T.; Langdon, J.; Lichtenstein, L.M.
Science 269, 688-690, 1995
A:Title: Molecular identification of an IGF-dependent histamine-releasing factor.
A:Reference number: A43082; MUID:9550660; PMID:7542803
A:Accession: A43082
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <MAC>
R:Ward, L.D.; Hong, J.; Whitehead, R.H.; Simpson, R.J.
Electrophoresis 11, 883-891, 1990
A:Title: Development of a database of amino acid sequences for human colon carcinoma
proteins separated by two-dimensional polyacrylamide gel electrophoresis.
A:Reference number: A33176; MUID:91176935; PMID:2079031
A:Accession: F33178
A:Status: preliminary

A:Molecule type: protein
A:Residues: 1-18 <MAR>
C:Genetics:
A:Gene: GDB:TPT1; TCTP
A:Cross-references: GDB:134697
A:Map position: 13q14.3-13q14.3
C:Superfamily: IGF-dependent histamine-releasing factor
C:Keywords: lymphocyte

Query Match 100.0%; Score 898; DB 1; Length 172;
Best Local Similarity 100.0%; Pred. No. 7,66-69;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MTIYEDLISHDMFSDIYKTRIELADGICLVEGKKNVSRTEGNIDSLIGGNASARGEGE	60
DB	1	MTIYEDLISHDMFSDIYKTRIELADGICLVEGKKNVSRTEGNIDSLIGGNASARGEGE	60
QY	61	GTESTVITGVDMVHHLDSTFTKEAYKKYIKDYMSIKGKLEBQRPFRVYFMTGAAE	120
DB	61	GTESTVITGVDMVHHLDSTFTKEAYKKYIKDYMSIKGKLEBQRPFRVYFMTGAAE	120
QY	121	QIKHILANFNKYQFFIGENNPDKGVALLDYREDOYTPPYMIFPKDGLMEKIC	172
DB	121	QIKHILANFNKYQFFIGENNPDKGVALLDYREDOYTPPYMIFPKDGLMEKIC	172

RESULT 2

S00775
IGF-dependent histamine-releasing factor - mouse
N:Alternate names: 21K tumor protein; tumor-associated protein
C:Species: Mus musculus (house mouse)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S00775
R:Chittipatia, S.T.; Makrides, S.; Bandyopadhyay, R.; Braerman, G.
Nucleic Acids Res. 16, 2350, 1988
A:Title: Nucleotide sequence of a major messenger RNA for a 21 kilodalton polypeptide
that is under translational control in mouse tumor cells.
A:Reference number: S00775; MUID:86189840; PMID:3357792
A:Accession: S00775
A:Molecule type: mRNA
A:Residues: 1-172 <CHI>
A:Cross-references: UNIPROT:P14701; EMBL:X06407; NID:g52848; PIDN:CAA29697.1;
PID:g52849
C:Superfamily: IGF-dependent histamine-releasing factor
C:Keywords: lymphocyte

Query Match 97.1%; Score 872; DB 1; Length 172;
Best Local Similarity 95.9%; Pred. No. 1,2e-66;
Matches 165; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY	1	MTIYEDLISHDMFSDIYKTRIELADGICLVEGKKNVSRTEGNIDSLIGGNASARGEGE	60
DB	1	MTIYEDLISHDMFSDIYKTRIELADGICLVEGKKNVSRTEGNIDSLIGGNASARGEGE	60
QY	61	GTESTVITGVDMVHHLDSTFTKEAYKKYIKDYMSIKGKLEBQRPFRVYFMTGAAE	120
DB	61	GTESTVITGVDMVHHLDSTFTKEAYKKYIKDYMSIKGKLEBQRPFRVYFMTGAAE	120
QY	121	QIKHILANFNKYQFFIGENNPDKGVALLDYREDOYTPPYMIFPKDGLMEKIC	172
DB	121	QIKHILANFNKYQFFIGENNPDKGVALLDYREDOYTPPYMIFPKDGLMEKIC	172

RESULT 3

A38956
IGF-dependent histamine-releasing factor - rabbit
N:Alternate names: 21K tumor protein; tumor-associated protein
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A38956